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(54) Title: METHODS FOR TESTING BIOLOGICAL NETWORK MODELS

(57) Abstract

The present invention provides methods and systems for testing and confirming how well a network model represents a biological pathway in a biological system. The network model comprises a network of logical operators relating input cellular constituents (e.g., mRNA or protein abundances) to output classes of cellular constituents, which are affected by the pathway in the biological system. The methods of this invention provide, first, for choosing complete and efficient experiments for testing the network model which compare relative changes in the biological system in response to perturbations of the network. The methods also provide for determining an overall goodness of fit the network model to biological system by: predicting from the network model how output classes behave in response to the chosen experiments, finding measures of relative change of cellular constituents actually observed in the chosen experiments, finding goodnesses of fit of each observed cellular constituent to an output class with which the cellular constituent has the strongest correlation, and determining an overall goodness of fit of the network model from the individual goodnesses of fit of each observed cellular constituent. Additionally, these methods provide for testing the significance of the overall goodness of fit according to a nonparametric statistical test using an empirically determined distribution of possible goodnesses of fit. This invention also provides for computer systems for carrying out the computational steps of these methods.